

FIG. 1.



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ABCG5	M	-----GDLSSLTPGGSMGLQVNRGSSQSSLEGAPAT-APEPHSLGILHASYSUSHRVR-PW-----	54
ABCG8	M	MAGKAAEERGLPKGATPQDTSGLQDRLFSSES DNSLYFTYSGQENTLEVRDLNYQVDLASQVWPWFELQLAQ	70
ABCG5	---	WDITSCRQQWTRQILKDVSLYVESGQIMCIIIGSSGSCKTTLLDAMSGRLGRAGTFL-GEVYVNGRA	119
ABCG8	FKMPMTSPSC-Q	NSCELGIQNL SFKVRSGQMLAIIIGSSGCGRASLLDVITGR-GHGGKIKSCQIWINGQP	136
ABCG5	LRREQFDQFSYMLQSDTLISSLTVRETIHYTALLAIRRG-NPGSFQKKVEAMAEISISHVADRLLIGNY	188	
ABCG8	SSPOLVRKQVAHVRQHNQLLPNLTVRETIATAQMRLPRTFSQAQRDKRVEDVIAEIRLRQCADTRVGNM	208	
ABCG5	SLGCIISTGERRRVSI	AAQLIQDPKVMLFDEPTTGLDCMTANQIIVLLVEIARRNRIVVLTIIHQPRSEIIFQ	258
ABDG8	YVRCLSGGERRRVSI	IGVQLIWNIGILILDEPTSGLDSTAHNLVKTL SRLAKGNRILVLSIHQPRSDIER	278
ABCG5	LFDKIAILSFCELTFCGTPAEMLDFFNDCCGYPCPEHSNPFDFYMDLTSVDTSKEREIEISKRVMIESA	328	
ABCG8	LFDLVLLMTSGTPIYILGAAQHMVQYETAIGYPCERYSNPADFVVDLTSIDRRSREOEIATREKAQSLAAL	348	
ABCG5	YDDSA-----	ICHKTIKNIERMKHLKT--IPM-----VPFKTKDSPGVFESKLGVLIRRVTRNLVRNKLAV	386
ABCG8	FLEKVRDLDDFLWKAETKDLDEDTCESSVTPLDNTNCLPSPTK-MPGAVQQFTTLIRROI SNDFRDLPTL	417	
ABCG5	ITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRVGLLYQVFATPYTGMINAVNLPVIRAVSDQESQDG	456	
ABCG8	LIHGAEACIMSMITIGE--LYFGHGSIQLSFMDTAALLFMIGALIEFNVIIDVISKCYSERAMLYYELEDG	485	
ABCG5	LYQKWQMMIAYAHVLPFSVVATMI	FSSVCYWTGLHPEVARFGYFSAALLAPHLIGEFLLTVLLGIVQN	526
ABCG8	LYTTGPGYFFAKIILGELPEHCAYIIIIYGMPTYWLANIRREGLOPELLHFLLVWLVFCCRIMALAAALLPT	555	

FIG. 1C.



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ABCG5 PNIIVSVVALLLSIAGVILVSGFLRNIIQEM-PIPFKIIISYFTFQKYCSSEITVVNEFYGLNFTCGSSNNVSVT 595
ABCG8 FHMASFESNALYNSFYLAGGEMINLSSLWTVB-AWISKVSELRWCHEGLMKIQFSRRTYKMPGLNLTIA 623

ABCG5 TNPMCAFTQGIQFIEKTCPGATSRFTMNFLILYSFIPALVIIGIVVFKIRDHLISR-- 651
ABCG8 VS-----GDKILSAMELDSYPLYAI-YLIVIGLSGGFMVLYYVSLRFIKQKPSQDW 673

Walker A Hotif
Walker B Hotif
Signature C-Hotif

ABCG5 Putative Transmembrane Domain
ABCG8 Putative Transmembrane Domain

FIG. 1C. (CONTINUED)



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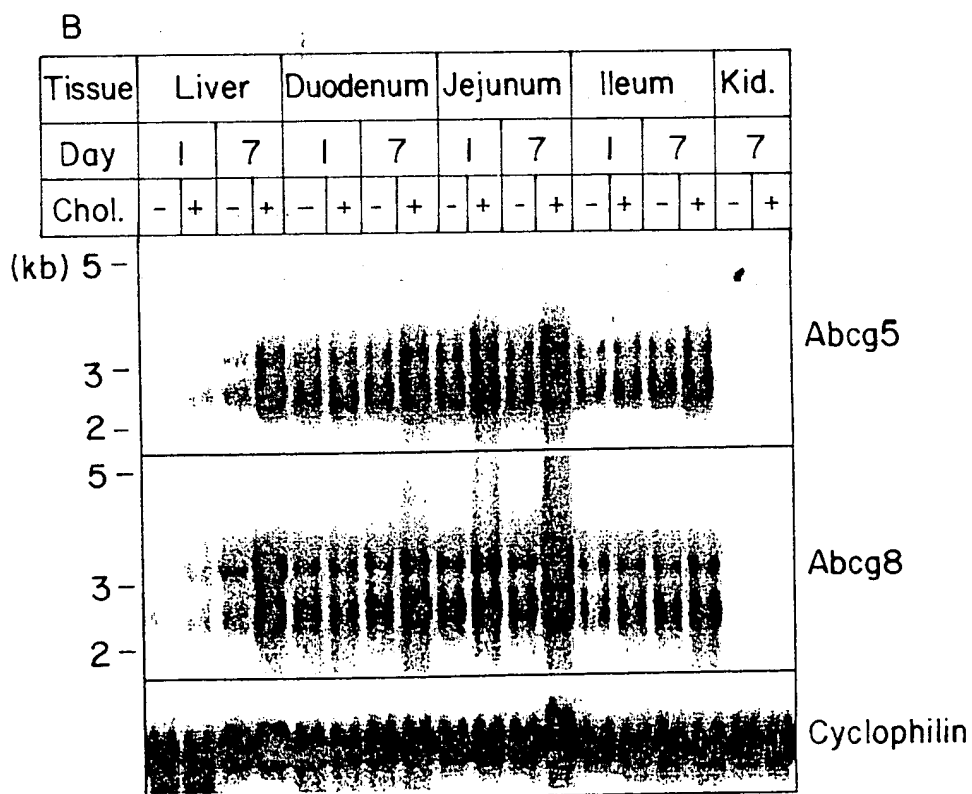
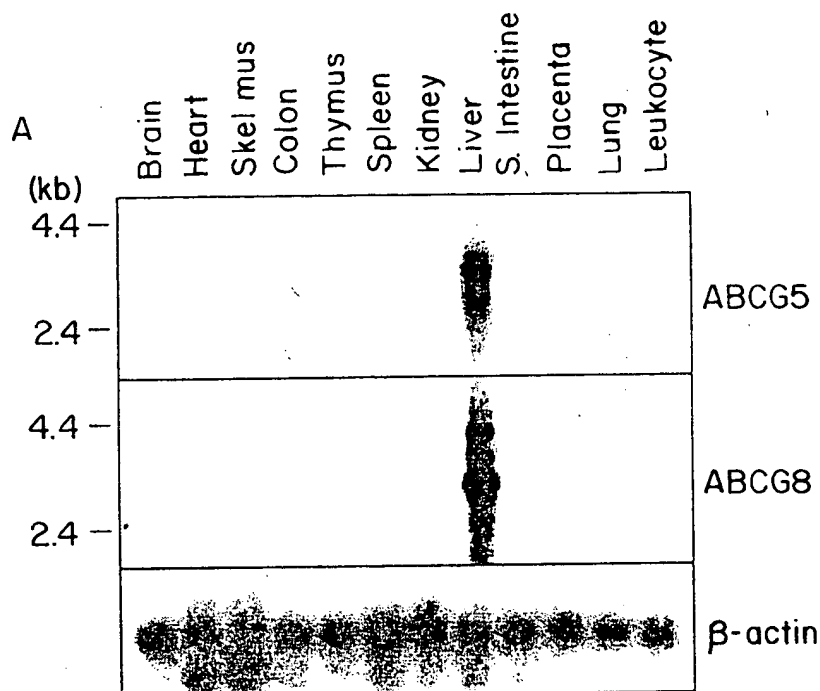


FIG. 2.

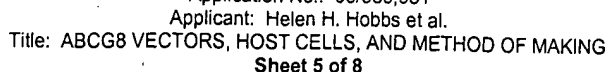
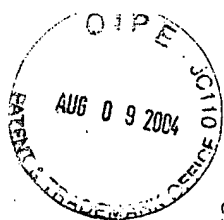
[illegible]

FIG. 3.

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gattttatactcactcaggaaggagcatcaaaagacgtagaaggaggtatttccccatagacgtctgcctcatggggattctga
cagcagagtgcctgtgctgtgtagtaggattgggtcaatctcaggcaatcctgtctccccatagaacaggggactgagggcgtcc
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FIG. 3. (CONTINUED)

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[illegible]

The 4 exons are underlined and the conserved regions are in uppercase. The sequence ends in intron 2 of ABCG5 and is in the following order:

ABC88	exon 2	(reverse strand)
ABC88	intron 1	(reverse strand)
ABC88	exon 1	(reverse strand)

FIG. 3. (CONTINUED)

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Gap between genes

ABCG5 exon 1 (forward strand)
ABCG5 intron 1 (forward strand)
ABCG5 exon 2 (forward strand)
ABCG5 intron 2 (forward strand, partial)

B. Sequence Between ABCG5 and ABCG8 Containing the Control Sequences

Gaccagtgtgttgtgccccttgtgtggtggcctcccctgctgtgtggcctctctgtctgtcttggctccttagagctggggcacctgag
ccctcctgtgtgccagccttTCTCCAGCATTCCTYCTGCGCAACACACTTCCTATAAACACACACCGTGTGTCTGCGCTATTGTCTGA
GATAAGGACACTCTGGCTAAAGGTACATCAGATAATGGCATCGTTGGCCAAatttggtgaactgttatctcacgaggattccaggg
ctgggtaggatcggacagggcactcccattggctcctcagttaaagctgcccctggagccggacagggccactagaaaaattcacttg
catttgcttcctgctagcc

FIG. 3. (CONTINUED)

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